location from Blimp1 staining. However, this study provides the first rough description of PGC migration in *M. domestica* and serves as a foundation for further experiments.

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Program/Abstract # 292
A molecular dynamics study on the Tre1 G protein-coupled receptor
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The Tre1 G protein-coupled receptor is required for proper germ cell migration in *Drosophila melanogaster*. In a severe partial loss-of-function allele of tre1, and tre1 sctt, the germ cells scatter across the posterior half of the embryo rather than forming two gonads. The molecular lesion in tre1 sctt is a point mutation that results in an in-frame deletion of eight amino acids, RYILIACH, which is located at the junction of the third transmembrane domain and second intracellular loop. The highly conserved arginine within this deleted region is critical for Tre1 function. However, it is not known whether the loss of these amino acids affect Tre1’s structure. The working hypothesis is that the amino acids RYILIACH are required to keep Tre1 in a fully functional conformation. As there is no crystal structure of Tre1 available, homology modeling of both wild-type Tre1 and Tre1 sctt was performed using the I-TASSER platform to generate three-dimensional structure predictions. These models have been further refined through the use of molecular dynamics simulations with the NAMD simulation package.

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Program/Abstract # 293
A crucial role for lipid phosphorylation in WntD-mediated primordial germ cell migration
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Although much work has been done characterizing genes controlling primordial germ cell (PGC) migration in *Drosophila* embryos, a major unanswered question is the identity of molecules providing guidance cues to these cells. We have previously demonstrated that the ligand WntD utilizes a β-catenin-independent pathway to control PGC migration, leading us to hypothesize that this novel signaling pathway could reveal insights into the mechanism of PGC guidance. We therefore undertook a suppressor screen to identify components of the WntD signaling pathway and discovered that loss of either CG16708, a putative ceramide kinase, or CG31873, a putative multi-substrate lipid kinase, suppresses WntD overexpression. Additionally, embryos double homozygous mutant for both kinase genes display a WntD mutant-like phenotype in primordial germ cell migration. We hypothesize that the WntD signaling pathway produces a phospholipid substrate that can be shaped into a gradient by phospholipid phosphatases Wun and Wun2, thus providing directional cues to migrating PGC.

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Program/Abstract # 294
*Xenopus* Nanos1 is required to preserve PGCs from endoderm specification
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A significant problem in development is how germ cell fate with its characteristics of totipotency is preserved in the context of somatic cell differentiation. Nanos is expressed in multipotent cells, stem cells, and primordial germ cells (PGCs) of organisms as diverse as jellyfish and humans. The only molecular role assigned to Nanos is as part of a translational repression complex with Pumilio. Here we show by loss-of-function experiments that *Xenopus* Nanos1 is required for PGC preservation. Knockdown of maternal Nanos1 resulted in a significant decrease in PGCs and loss of germ cells from the gonads. Nanos1 mutant embryos were rescued by coinjection of Nanos1 message, indicating the specificity of the morpholino. PGCs deficient in Nanos1 inappropriately express somatic genes such as Xsox17-alpha and Bix4, essential for endoderm specification. Furthermore, whereas normal PGCs do not become transcriptionally active until neurula, Nanos1 depleted PGCs express Xsox17-alpha by stage 10, similar to when somatic endoderm initiates their expression. Consistent with this premature gene transcription, PGCs now express a hyperphosphorylated RNA Pol II-CTD. Lineage tracing and TUNEL staining revealed that Nanos1 deficient PGCs fail to migrate out of the endoderm. They appear to undergo apoptosis rather than convert to normal endoderm. We propose that Nanos1 functions to translationally repress RNAs that normally specify endoderm and promote apoptosis, thus preserving the germ line. This work was supported by the NIH grant GM33932 to MLK.

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Program/Abstract # 295
Oskar predates the evolution of insect germ plasm
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Oskar is the only gene known to be both necessary and sufficient for germ cell specification in *Drosophila melanogaster*. However, despite this essential function, oskar has thus far only been found in the genomes of holometabolous insects that specify their germ line through the inheritance of a specialized cytoplasm termed “germ plasm.” Using high-throughput transcriptome sequencing, we have identified an ortholog of oskar from the cricket Gryllus bimaculatus, a hemimetabolous insect that is thought to retain ancestral characteristics of insect oogenesis and embryogenesis. Like all crickets and grasshoppers, Gryllus lacks germ plasm and appears to specify its germ cells inductively during mid-embryogenesis. Gb-oskar is expressed at high levels in ovaries, consistent with a conserved function in oogenesis, but does not localize within oocytes or to developing germ cells in embryos. We are currently working to determine the function of Gb-oskar using RNAi. The study of oskar from a basally-branching insect will provide insight into the evolutionary origins of this gene, and may shed light on the evolution of germ plasm in insects.

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Program/Abstract # 296
Ultrastructure of putative germ plasm in penaeid shrimp
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